

Result No.	Score	Query	Match	length	DB	ID	Description
1	415	81.7	3208	9	US-10-214-811-27		Sequence 27, Appl
2	415	81.7	3208	10	US-09-780-016-27		Sequence 27, Appl
3	386.8	76.1	476	9	US-09-918-995-17191		Sequence 1191, A
4	316.6	62.3	380	10	US-09-960-352-4677		Sequence 4677, A
c	5	272.8	53.7	418	9	US-09-962-436-220	Sequence 220, Appl
6	205.8	40.5	439	9	US-09-918-995-14771		Sequence 14771, A
7	191	37.6	202	10	US-09-815-343-1466		Sequence 1466, Appl
8	173	34.1	390	10	US-09-770-791-20		Sequence 20, Appl
9	76.4	15.0	271	10	US-09-294-093B-735		Sequence 735, Appl
10	76	15.0	836	10	US-09-764-864-39		Sequence 39, Appl
11	76	15.0	836	10	US-09-764-864-498		Sequence 498, Appl
c	12	74	342	10	US-09-826-312-7		Sequence 7, Appl
13	73	14.4	359	10	US-09-876-574-2188		Sequence 2188, Appl
14	70	13.8	331	9	US-09-933-797-112		Sequence 112, App
15	58.6	11.5	612	9	US-09-796-692-8547		Sequence 8547, Ap
16	58.6	11.5	612	9	US-10-040-862-8547		Sequence 8547, Ap
17	52.8	10.4	269	10	US-09-876-574-15085		Sequence 15085, A
18	41.8	8.2	22118	9	US-09-799-462A-16		Sequence 16, Appl
19	41.8	8.2	22118	9	US-10-125-767-16		Sequence 16, Appl

20	41.8	8.2	22118	9	US-09-815-981-5	Sequence 5, Appl
21	41.8	8.2	22118	9	US-09-836-918A-16	Sequence 16, Appl
22	41.8	8.2	22118	9	US-09-815-979-5	Sequence 5, Appl
23	41.8	8.2	22118	9	US-10-151-081-16	Sequence 16, Appl
24	40.4	8.0	479	9	US-09-918-999-9339	Sequence 9339, App
25	40.4	8.0	9539	9	US-10-239-676-52	Sequence 52, Appl
26	40.2	7.9	431	10	US-09-960-352-5558	Sequence 5558, App
27	39.6	7.8	14649	9	US-10-239-676-121	Sequence 121, App
28	39.4	7.8	15732	9	US-10-239-676-95	Sequence 95, Appl
29	39.2	7.7	13485	9	US-10-125-540-5448	Sequence 548, App
30	39.2	7.7	13485	10	US-09-764-870-548	Sequence 548, App
31	39	7.7	286	10	US-09-960-352-13342	Sequence 13342, Sequence 12412,
32	38.6	7.6	314	10	US-09-960-352-12412	Sequence 4765, App
33	38.6	7.6	495	10	US-09-878-574-4765	Sequence 1, Appl
34	38.6	7.6	2807	10	US-09-940-836A-1	Sequence 109, App
35	38.2	7.5	7903	9	US-10-239-676-109	Sequence 872, App
36	38	7.5	4677	10	US-09-834-975-872	Sequence 872, App
37	38	7.5	4677	10	US-09-834-975-873	Sequence 884, App
38	38	7.5	4677	10	US-09-834-975-884	Sequence 161, App
39	37.8	7.4	758	10	US-09-764-853-161	Sequence 15443, A
40	37.6	7.4	461	9	US-09-918-999-15443	Sequence 5927, App
41	37.4	7.4	459	10	US-09-867-701-5927	Sequence 55, Appl
42	37.4	7.4	7802	9	US-10-239-676-55	Sequence 160, App
43	37.4	7.4	9515	9	US-10-239-676-160	Sequence 4630, App
44	37	7.3	327	10	US-09-960-352-1630	Sequence 131, App
45	37	7.3	698	9	US-10-091-483-131	

194 CTTCTCAGCAGCTGTACTGTCCATC

194 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTACCATGCTTTCACCTTCCACT 253

Db	2885	CTAATTGAGAAAGTAGTACTGCTGGATGGGAGGTGTGTAAACCATGCTTTTCACTTCCACT	2944
OY	254	GCATCTTCGCTTGGCTTCAAAAACGACAGAGTGTGTCCATTGGACAACAGAGAGTGGAT	313
Db	2945	GCATCTCTCCCTGGCTCAAAAACGACGACAGTGTGTCCATTGGACAACAGAGAGTGGANT	3004
OY	314	TCCAAAAGTGTGGGCACTGGGAAAAGACATCTTCCATCATCAAGCTTAATGTTTGTATTTC	373
Db	3005	TCCAAAAGTATGGGCACTGGGAAAAGACATCTTCCATCATCAAGCTTAATGTTTGTATTTC	3064
OY	374	ATTTAATGACTTTCCTGCTGTTTACTTAATTACAATTTGATGGAGACTGTGTTTTTTC	433
Db	3065	ATTTAA-TGACTTTCCTGCTGTTTACTTAATTACAATTTGATGGAGACTGTGTTTTTTC	3123
OY	434	TGCTTTGTTTTTTCAGTTTGTCTGTCTGTAGCCATATTGTATCTGTGTCAAAATAAGT	493
Db	3124	TGCTTTGTTTTTTCAGTTTGTCTGTCTGTAGCCATATTGTATCTGTGTCAAAATAAGT	3183
OY	494	CCAGTTGGATTCTGG 508	
Db	3184	CCAGTTGGATTCTGG 3198	

```

RESULT 2
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. US20020004591A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abulu, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020004591A1el Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-780-016-27

```

Query Match	81.7%	Score 415	DB 10	Length 3208
Best Local Similarity	98.6%	Pred. No. 3.8e-110		
Matches 429	Conservative	0	Mismatches 5	Indels 1
			Gaps	1
QY	74	AAATGAAAAAGTGCAGATGCAGTACCCCTCGTGGCCCTGGGATATGTGGTAACTGTCG	133	
Db	2765	AAAAAAAAAATGGAATCCATACCCCTCTGGCCCTGGGATATTTGGTGAATACTGTG	2824	
QY	134	CCATCTGCAGGACACCATTTATGGATCTTTGCATAGAAATGTCMAAGCTAACCGAGGGCTCG	193	
Db	2825	CCATCTCAGAGAACACCATTTATGGATCTTTGCATAGAAATGTCMAAGCTAACCGAGGGCTCG	2884	
QY	194	CTATTTCAGAAAGATGTAACTGTCCGATCGGGGAGATCTGTAAACATGCTTTTCACTTCCACT	253	
Db	2885	CTATTTCAGAAAGATGTAACTGTCCATGCGGAGATCTGTAAACATGCTTTTCACTTCCACT	2944	
QY	254	GCACTCTCGCTGGCTCAAAAACAGACAGAGTGCTGTCCATTGGACAACAGAGAGTGGGAT	313	
Db	2945	GCACTCTCGCTGGCTCAAAAACAGACAGAGTGCTGTCCATTGGACAACAGAGAGTGGGAT	3004	
QY	314	TCCAAAAGTATGGCACATAGAAAAGATTCCTTCATCAAGCTTAATTTGTTTGTATTTC	373	

Db	3005	TCCAAGATGAGGCACTAGAGAAAGACTTTCATCAAGCTTAATTGTTTGTATTTC	3066
QY	374	ATTTAATGACTTTCCCTGCTGTTACCTAATTACAAATTGGATGGAACGTGTTTTTTC	433
Db	3065	ATTTAA-TGACTTTCCTGCTGTTACCTAATTACAAATGGATGGAACGTGTTTTTTC	3122
QY	434	TGCTTGTTTTTTCAGTTTGCCTGTTTCTGTAGCCATTTGTATTCTGTGTCAATAAAGT	493
Db	3124	TGCTTGTTTTTTCAGTTTGCCTGTTTCTGTAGCCATTTGTATTCTGTGTCAATAAAGT	3183
QY	494	CCAGTGGATTCTGG 508	
Db	3184	CCAGTGGATTCTGG 3198	

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RESULT 3
US-09-918-995-17191
; Sequence 17191, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17191
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-17191

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Query Match	76.1% ; Score 386.8 ; DB 9 ; Length 476 ;
Best Local Similarity	98.8% ; Pred. No.2.le-102 ;
Matches 399 ;	Conservative 0 ; Mismatches 4 ; Indels 1 ; Gaps 1 ;
QY 9	GGCGCAGCGCATGCGATGCGATGCGATACCCCGACGGCGGCACCAACAGCGCGCGCGGCAAGAGCG 68
Db 74	GGCGCGCAGCGCATGCGATGCGATGCGATACCCCGACGGCGGCACCAACAGCGCGCGCGGCAAGAGCG 133
QY 69	CTTTGAAGTGAAGAAAGTGGAAATGCAATGACCTCTGCGGCGCTGGGATATTGTGTGATGA 128
Db 134	CTTTGAAGTGAAGAAAGTGGAAATGCAATGACCTCTGCGGCGCTGGGATATTGTGTGATGA 193
QY 129	CTGTGCACATCGCAGGAACACACATTAATGATCTTTGCAATGATGTCAGATGTCAGATTAACGACGCG 188
Db 194	CTGTGCACATCGCAGGAACACACATTAATGATCTTTGCAATGATGTCAGATGTCAGATTAACGACGCG 253
QY 189	GTCGCGTACTTCAGAAAGAGTGTACTGTGCAATGGGAGCTGTGAACCATGCTTTTCACATT 248
Db 254	GTCGCGTACTTCAGAAAGAGTGTACTGTGCAATGGGAGCTGTGAACCATGCTTTTCACATT 313
QY 249	CCACTGCATCTCTGGCTGGCTCCAAAACGACGAGTGTGTCATTTGGGACCAACAGAGAGTG 308
Db 314	CCACTGCATCTCTGGCTGGCTCCAAAACGACGAGTGTGTCATTTGGGACCAACAGAGAGTG 373
QY 309	GGAAATTCAAAAGATGATGGGCACTAGAGAAAACATCTCTCCATCAAGCTTTAAATTTTGTGT 368
Db 374	GGAAATTCAAAAGATGATGGGCACTAGAGAAAACATCTCTCCATCAAGCTTTAAATTTGTTGG 433
QY 369	TATTCATTTAATTAAGCTTTCCCTGCTGTTACCTAATTAACAATT 412
Db 434	TATTCATTTAATTAAGCTTTCCCTGCTGTTACCTAATTAACAATT 476

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RESULT 4
US-09-960-352-4677
; Sequence 4677, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Mengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4677
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7
US-09-960-352-4677

Query Match          62.3%; Score 316.6; DB 10; Length 380;
Best Local Similarity 94.2%; Pred. No. 4.5e-82;
Matches 340; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

QY 14 CACGATGATGTGATACCCGAGGCGACCAACAGCGGCGGCGGAGAGAGCGCTTG 73
DB 2 CACGATGATGTGATACCCGAGGCGACCAACAGCGGCGGCGGAGAGAGCGCTTG 61
QY 74 AAGTGAAGAAAGTGAATGACAGTACCCCTGCGCTGGGCTGGGATATGTGTTGATTAAGTGTG 133
DB 62 AAGTGAAGAAAGTGAATGACAGTACCCCTGCGCTGGGCTGGGATATGTGTTGATTAAGTGTG 121
QY 134 CCATCTGCAGAGAACACCATATTATGATCTTTCATAGATGTCAAGCTAACAGCGCTCG 193
DB 122 CCATCTGCAGAGAACACCATATTATGATCTTTCATAGATGTCAAGCTAACAGCGCTCG 181
QY 194 CTACTTCAGAGAGTGTACTGTGATGGGAGTGTCTATACCATATGCTTTTCACTTCCACT 253
DB 182 CTACTTCAGAGAGTGTACTGTGATGGGAGTGTCTATACCATATGCTTTTCACTTCCACT 241
QY 254 GCATCTCTCGCTGGCTCAAAAACAGAGGTGTGTCCATTGGACACAGAGAGTGGGAAT 313
DB 242 GCATCTCTCGCTGGCTCAAAAACAGAGGTGTGTCCATTGGACACAGAGAGTGGGAAT 301
QY 314 TCCAAAGTATGGGCACTAGAGAA--AGACTTCTTCATCAAGCTTAATGTTTGTAT 371
DB 302 TCCAAAGTATGGGCACTAGAGAAAGAGAAATCTTCGATTAAGCTCAACTGTTTGTGT 361
QY 372 T 372
DB 362 T 362

RESULT 5
US-09-962-436-220/c
; Sequence 220, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 220
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; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-220

Query Match          53.7%; Score 272.8; DB 10; Length 418;
Best Local Similarity 86.0%; Pred. No. 2.5e-69;
Matches 349; Conservative 0; Mismatches 52; Indels 5; Gaps 4;

QY 101 TCTGGGCTGGGATATGTGTGATATACGTGTGATCTGCAGAACCATATATGATC 160
DB 417 TCTGGGCTGGGATATGTGTGATATACGTGTGATCTGCAGAACCATATATGATC 358
QY 161 TTTCATAGATAGTCAAGCTAACAGCGCCGCTTACCTTGAAGAGTACTTCCGAT 220
DB 357 --TGCATTAATGTCAAGCTAACAGAGTCTGCACCTTGAAGAGTGTACCTTCAC 300
QY 221 GGGAGTCTGTAAACAGCTTTTCACTTCCAGTACGTCTCTCGTGGCTCAAAACAGAC 280
DB 299 GGGAGCTGTAAACAGCTTTTCACTTCCAGTACGTCTCTCGTGGCTCAAAACAGAC 241
QY 281 AGGTGTCTCATTTGAGAACAGAGAGTGGGAATTCCAAAGTATGGGCACTAGAGAAAGA 340
DB 240 AGGTGTCTCATTTGAGAACAGAGAGTGGGAATTCCAAAGTATGGGCACTAGAGAAAGA 181
QY 341 CTCTTCATCAAGCTTAATGTTTGTATATCAATTAATGACTTCCCTGCTTACC 400
DB 180 ATCTTCATCAAGCTTAATGTTTGTATATCAATTAATGACTTCCCTGCTTACC 122
QY 401 TAATTAACAATTTGATGAGAACTGTGTTTCTGCTTTGTTTTCAGTTGCTGTTTC 460
DB 121 TAATTAACAATTTGATGAGAACTGTGTTTCTGCTTTGTTTTCAGTTGCTGTTTC 63
QY 461 TGTAGCATATGTATTTCTGTCTCAATTAAGTCCATTTGATCT 506
DB 62 CGCAGCCACATTTGATTTCTGTCAATAAAGTCCATTTGATCT 17

RESULT 6
US-09-918-995-14771
; Sequence 14771, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14771
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-14771

Query Match          40.5%; Score 205.8; DB 9; Length 439;
Best Local Similarity 99.0%; Pred. No. 7.5e-50;
Matches 207; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 84 GTGGAATGACAGTACGCTCTGCGGCTGTGGATATTTGTGTTGATTAATGATGCTATCAG 143
DB 231 GTGGAATGACAGTACGCTCTGCGGCTGTGGATATTTGTGTTGATTAATGATGCTATCAG 290
QY 144 GAACCAATTAATGATTTTGCATAGATGCAAGCAAGCAAGCAAGCGCCGCTACTTACA 203
DB 291 GAACCAATTAATGATTTTGCATAGATGCAAGCAAGCAAGCAAGCGCCGCTACTTACA 350
QY 204 AGAGTACTGTGCAATGGGAGTCTGTAAACATGCTTTTCACTTCCAGTCACTCTCTCG 263
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Db	351	AGAGTGTACGTCGGCATTGGGGAGCTCTTAACCATGCCTTTCACTTCATCGACTCTTCG	410
Qy	264	CTGGCTCAAACAACGACAGTGTTGTCAT 	292
Db	411	CTGGCTCAAACAACGACAGTGTTGTCAT	439

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RESULT 7
US-09-815-343-1466
: Sequence 1466, Application US/09815343
: Patent NO. US20010055596A1
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815.343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ. ID NOS: 1556
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 1466
LENGTH: 202
TYPE: DNA
ORGANISM: Homo sapien
US-09-815-343-1466

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RESULT 8
US-09-770-791-20
: Sequence 20, Application US/09770791
: Patent No. US20020062014A1
: GENERAL INFORMATION:
: APPLICANT: Gorlach, Jorn
: APPLICANT: An, Yong-Qiang
: APPLICANT: Hamilton, Carol M.
: APPLICANT: Price, Jennifer L.
: APPLICANT: Raines, Tracy M.
: APPLICANT: Yu, Yang
: APPLICANT: Rameaka, Joshua G.
: APPLICANT: Page, Amy
: APPLICANT: Matthew, Abraham V.
: APPLICANT: Ledford, Brooke L.
: APPLICANT: Woessner, Jeffrey P.
: APPLICANT: Haas, William David
: APPLICANT: Garcia, Carlos A.
: APPLICANT: Kricker, Maya
: APPLICANT: Slader, Ted
: APPLICANT: Davis, Keith R.
: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurban, Patrick

```

```

: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
:
: TITLE OF INVENTION: thaliana
:
: FILE REFERENCE: 2029 (PARA-018PRV)
:
: CURRENT APPLICATION NUMBER: US/09/770,791
:
: CURRENT FILING DATE: 2001-01-26
:
: PRIOR APPLICATION NUMBER: 60/178,480
:
: PRIOR FILING DATE: 2000-01-27
:
: NUMBER OF SEQ ID NOS: 999
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 20
:
: LENGTH: 390
:
: TYPE: DNA
:
: ORGANISM: Arabidopsis thaliana
:
US-09-770-791-20

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RESULT 9
US-09-294-093B-735
; Sequence 735, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASS
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 735
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700343233H1
; NAME/KEY: unsure
; LOCATION: 89, 219
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-735
Query Match 15.0%; Score 76.4; DB 10; Length 271;
Best Local Similarity 70.6%; Pred. No. 2,2e-12;
Matches 115; Conservative 0; Mismatches 47; Indels 1; Gaps 1;
y 25 GTGATATCCCGAGCGGACACACAGCGGCGGCAAGAAGCGCTTTGAGTGAAGAAG 84

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Db 110 GTGGTCGCTCCCTCCCTCCATCCCTCCGCAAGCCCAACAGCGCTTCAGATCAAGAAG 169
Qy 85 TGAATGACGATGACCCCTGGGCGCTGGATATTTGGTTGATTAACGTCCATCTCCAG 144
Db 170 TGAACGCGCGCTGCGCTCTGGGCAATGGATATGCTGTCAGCA-TGGCCNATCTGCGC 228
Qy 145 AACCAATATGATCTTTGATAGATGTAACAGTCAAGTCAAG 187
Db 229 AACCAATATGATCTTTGATAGATGTAACAGTCAAGTCAAG 271

RESULT 10

US-09-764-864-39
; Sequence 39, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 39
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-39

Query Match 15.0%; Score 76; DB 10; Length 836;
Best Local Similarity 55.9%; Pred. No. 5.4e-12;
Matches 170; Conservative 0; Mismatches 125; Indels 9; Gaps 1;

Qy 32 CCCCCGCGGCGCACCAACAGCGCGGCGGCAAGCGCTTTGAAGTGAAGTGAAGTGA 91
Db 65 CCGGAGAGCTCAGGCTCCCAAGTGGGAGCGGCAAGATGTTCCCTCAAGAGTGGAGC 124
Qy 92 CAGTAGCCCTCTGGGCGCTGGATATTTGATGATGATGATGATGATGATGATGATGAT 151
Db 125 CCGTGGCCATGTGAGAGTGGAGCTGGAGTGGATGCGATGCGGCACTCCAGGCTCAG 184
Qy 152 TTATGATCTTTGATAGATGTAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 211
Db 185 TGATGATCTCTGTTTAAATGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 235
Qy 212 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
Db 236 TTGTGCTGTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 295
Qy 272 AAACAGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 331
Db 296 AACAGACAGATGCTGCTCTCTCTGCGACAGAGAGTGGTGGTCCAAAGATGCGAAT 355
Qy 332 AGCA 335
Db 356 GAGA 359

RESULT 11

US-09-764-864-498
; Sequence 498, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 498
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (45)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-498

Query Match 15.0%; Score 76; DB 10; Length 836;
Best Local Similarity 55.9%; Pred. No. 5.4e-12;
Matches 170; Conservative 0; Mismatches 125; Indels 9; Gaps 1;

Qy 32 CCCCCGCGGCGCACCAACAGCGCGGCGGCAAGCGCTTTGAAGTGAAGTGAAGTGA 91
Db 118 CCGGAGAGCTCAGGCTCCCAAGTGGGAGCGGCAAGATGTTCCCTCAAGAGTGGAGC 177
Qy 92 CAGTAGCCCTCTGGGCGCTGGATATTTGATGATGATGATGATGATGATGATGATGAT 151
Db 178 CCGTGGCCATGTGAGAGTGGAGCTGGAGTGGATGCGATGCGGCACTCCAGGCTCAG 237
Qy 152 TTATGATCTTTGATAGATGTAACAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 211
Db 238 TGATGATCTCTGTTTAAATGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 288
Qy 212 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
Db 289 TTGTGCTGTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 348
Qy 272 AAACAGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 331
Db 349 AACAGACAGATGCTGCTCTCTCTGCGACAGAGAGTGGTGGTCCAAAGATGCGAAT 408
Qy 332 AGCA 335
Db 409 GAGA 412

RESULT 12

US-09-826-312-7
; Sequence 7, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianlie
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/826,312
; PRIORITY FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-312-7

Query Match 14.6%; Score 74; DB 10; Length 342;
Best Local Similarity 58.4%; Pred. No. 1.3e-11;
Matches 153; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

Qy 58 GGCAGAGCGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 117
Db 76 GCGGACAGATGTTTCCCTCAAGAGTGGAGACCGGCTGGCCATGTGGAGCTGGAGCTG 135
Qy 118 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 177
Db 136 GAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 195

